



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: 15966-776CIP

is a patent application of

GERLACH, VALERIE L. et al.

Serial No. 09/898,570

Filed: July 3, 2001

For: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
USING THE SAME

STATEMENT TO SUPPORT FILING AND SUBMISSION IN
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

Sir:

In connection with a Sequence Listing submitted concurrently
herewith, the undersigned hereby states that:

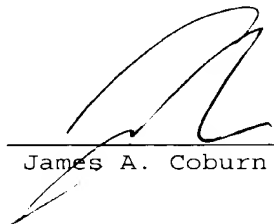
1. the submission, filed herewith in accordance with 37
C.F.R. § 1.821(g), does not include new matter;
2. the content of the attached paper copy and the
attached computer readable copy of the Sequence Listing, submitted in
accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same;
and
3. all statements made herein of their own knowledge are
true and that all statements made on information and belief are believed to
be true; and further, that these statements were made with the knowledge
that willful false statements and the like so made are punishable by fine
or imprisonment, or both, under Section 1001 of Title 18 of the United

Serial No. 09/898,570

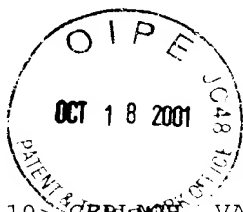
States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

Oct. 1, 2001
Date


James A. Coburn

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SEQUENCE LISTING

<110> GERLACH, VALERIE L.
ELLERMAN, KAREN
MACDOUGALL, JOHN R.
SMITHSON, GLENNDA

<120> NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
METHODS OF USING THE SAME

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 Pro Gly Ser Phe Gln Cys Leu Cys His Arg Gly Tyr Leu Leu Tyr Gly
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Pro Cys Ser Glu Cys Gln Val Thr Phe Ile His Leu Lys Cys Asp Ser
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 Gly Gln Cys Pro Pro Gly Gln His Ser Val Asp Gly Phe Lys Pro Cys
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<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX

Z97832_B.0.707

<400> 12

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Asp Asn Gln His Thr Cys Ile Gln Arg Pro Glu Glu Gly Met Asn Cys
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Met Asn Lys Asn His Gly Cys Ala His Ile Cys Arg Glu Thr Pro Lys
          35                      40                      45

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Gly Gly Ile Ala Cys Glu Cys Arg Pro Gly Phe Glu Leu Thr Lys Asn
  50                      55                      60

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Gln Arg Asp Cys Lys Leu Thr Cys Asn Tyr Gly Asn Gly Gly Cys Gln
  65                      70                      75                      80

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His Thr Cys Asp Asp Thr Glu Gln Gly Pro Arg Cys Gly Cys His Ile
          85                      90                      95

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```

Lys Phe Val Leu His Thr Asp Gly Lys Thr Cys Ile Gly Glu Arg Arg
          100                      105                      110

```

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Leu Glu Gln His Ile Pro Thr Gln Ala Val Ser Asn Glu Thr Cys Ala
          115                      120                      125

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Val Asn Asn Gly Gly Cys Asp Ser Lys Cys His Asp Ala Ala Thr Gly
          130                      135                      140

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Val His Cys Thr Cys Pro Val Gly Phe Met Leu Gln Pro Asp Arg Lys
          145                      150                      155                      160

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Thr Cys Lys Asp Ile Asp Glu Cys Arg Leu Asn Asn Gly Gly Cys Asp
          165                      170                      175

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His Ile Cys Arg Asn Thr Val Gly Ser Phe Glu Cys Ser Cys Lys Lys
          180                      185                      190

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Gly	Tyr	Lys	Leu	Leu	Ile	Asn	Glu	Arg	Asn	Cys	Gln	Asp	Ile	Asp	Glu	195	200	205
Cys	Ser	Phe	Asp	Arg	Thr	Cys	Asp	His	Ile	Cys	Val	Asn	Thr	Pro	Gly	210	215	220
Ser	Phe	Gln	Cys	Leu	Cys	His	Arg	Gly	Tyr	Leu	Leu	Tyr	Gly	Ile	Thr	225	230	235
His	Cys	Gly	Asp	Val	Asp	Glu	Cys	Ser	Ile	Asn	Arg	Gly	Gly	Cys	Arg	245	250	255
Phe	Gly	Cys	Ile	Asn	Thr	Pro	Gly	Ser	Tyr	Gln	Cys	Thr	Cys	Pro	Ala	260	265	270
Gly	Gln	Gly	Arg	Leu	His	Trp	Asn	Gly	Lys	Asp	Cys	Thr	Glu	Pro	Leu	275	280	285
Lys	Cys	Gln	Gly	Ser	Pro	Gly	Ala	Ser	Lys	Ala	Met	Leu	Ser	Cys	Asn	290	295	300
Arg	Ser	Gly	Lys	Lys	Asp	Thr	Cys	Ala	Leu	Thr	Cys	Pro	Ser	Arg	Ala	305	310	315
Arg	Phe	Leu	Pro	Glu	Ala	Ala	Val	Leu	Ser	Ile	Lys	Gln	Arg	Ala	Ser	325	330	335
Phe	Lys	Ile	Lys	Asp	Ala	Lys	Cys	Arg	Leu	His	Leu	Arg	Asn	Lys	Gly	340	345	350
Lys	Thr	Glu	Glu	Ala	Gly	Arg	Thr	Thr	Gly	Pro	Gly	Gly	Ala	Pro	Cys	355	360	365
Ser	Glu	Cys	Gln	Val	Thr	Phe	Ile	His	Leu	Lys	Cys	Asp	Ser	Ser	Arg	370	375	380
Lys	Gly	Lys	Gly	Arg	Arg	Ala	Arg	Thr	Pro	Pro	Gly	Lys	Glu	Val	Thr	385	390	395
Arg	Leu	Thr	Leu	Glu	Leu	Glu	Ala	Glu	Val	Arg	Ala	Glu	Glu	Thr	Thr	405	410	415
Ala	Ser	Cys	Gly	Leu	Pro	Cys	Leu	Arg	Gln	Arg	Met	Glu	Arg	Arg	Leu	420	425	430
Lys	Gly	Ser	Leu	Lys	Met	Leu	Arg	Lys	Ser	Ile	Asn	Gln	Asp	Arg	Phe	435	440	445
Leu	Leu	Arg	Leu	Ala	Gly	Leu	Asp	Tyr	Glu	Leu	Ala	His	Lys	Pro	Gly	450	455	460
Leu	Val	Ala	Gly	Glu	Arg	Ala	Glu	Pro	Met	Glu	Ser	Cys	Arg	Pro	Gly	465	470	475
Gln	His	Arg	Ala	Gly	Thr	Lys	Cys	Val	Ser	Cys	Pro	Gln	Gly	Thr	Tyr	485	490	495

Tyr His Gly Gln Thr Glu Gln Cys Val Pro Cys Pro Ala Gly Thr Phe
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 Gln Glu Arg Glu Gly Gln Leu Ser Cys Asp Leu Cys Pro Gly Ser Asp
 515 520 525
 Ala His Gly Pro Leu Gly Ala Thr Asn Val Thr Thr Cys Ala Gly Gln
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 Cys Pro Pro Gly Gln His Ser Val Asp Gly Phe Lys Pro Cys Gln Pro
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 Cys Pro Arg Gly Thr Tyr Gln Pro Glu Ala Gly Arg Thr Leu Cys Phe
 565 570 575
 Pro Cys Gly Gly Gly Leu Thr Thr Lys His Glu Gly Ala Ile Ser Phe
 580 585 590
 Gln Asp Cys Asp Thr Lys Val Gln Cys Ser Pro Gly His Tyr Tyr Asn
 595 600 605
 Thr Ser Ile His Arg Cys Ile Arg Cys Ala Met Gly Ser Tyr Gln Pro
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 Asp Phe Arg Gln Asn Phe Cys Ser Arg Cys Pro Gly Asn Thr Ser Thr
 625 630 635 640
 Asp Phe Asp Gly Ser Thr Ser Val Ala Gln Cys Lys Asn Arg Gln Cys
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 Gly Gly Glu Leu Gly Glu Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr
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 Pro Gly Asn Tyr Pro Ala Gly Val Glu Cys Ile Trp Asn Ile Asn Pro
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 Pro Pro Lys Arg Lys Ile Leu Ile Val Val Pro Glu Ile Phe Leu Pro
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 Ser Glu Asp Glu Cys Gly Asp Val Leu Val Met Arg Lys Asn Ser Ser
 705 710 715 720
 Pro Ser Ser Ile Thr Thr Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro
 725 730 735
 Ile Ala Phe Thr Ala Arg Ser Arg Lys Leu Trp Ile Asn Phe Lys Thr
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 Ser Glu Ala Asn Ser Ala Arg Gly Phe Gln Ile Pro Tyr Val Thr Tyr
 755 760 765
 Asp Glu Asp Tyr Glu Gln Leu Val Glu Asp Ile Val Arg Asp Gly Arg
 770 775 780
 Leu Tyr Ala Ser Glu Asn His Gln Glu Ile Leu Lys Asp Lys Lys Leu
 785 790 795 800

Ile Lys Ala Phe Phe Glu Val Leu Ala His Pro Gln Asn Tyr Phe Lys
805 810 815

Tyr Thr Glu Lys His Lys Glu Met Leu Pro Lys Ser Phe Ile Lys Leu
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Leu Arg Ser Lys Val Ser Ser Phe Leu Arg Pro Tyr Lys
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<210> 13

<211> 4550

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
Z97832_B_1

<400> 13

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<211> 974

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
Z97832_B_1

<400> 14

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Cys Val Glu Gly Thr Asp Asn Cys His Ile Asp Ala Ile Cys Gln Asn
  35                      40                      45

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Gly	Lys	His	Cys	Lys	Asp	Val	Asp	Glu	Cys	Glu	Arg	Glu	Asp	Asn	Ala	
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Gly	Cys	Val	His	Asp	Cys	Val	Asn	Ile	Pro	Gly	Asn	Tyr	Arg	Cys	Thr	
				85					90					95		
Cys	Tyr	Asp	Gly	Phe	His	Leu	Ala	His	Asp	Gly	His	Asn	Cys	Leu	Asp	
			100					105					110			
Val	Asp	Glu	Cys	Ala	Glu	Gly	Asn	Gly	Gly	Cys	Gln	Gln	Ser	Cys	Val	
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Asn	Met	Met	Gly	Ser	Tyr	Glu	Cys	His	Cys	Arg	Glu	Gly	Phe	Phe	Leu	
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Ser	Asp	Asn	Gln	His	Thr	Cys	Ile	Gln	Arg	Pro	Glu	Glu	Gly	Met	Asn	
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Cys	Met	Asn	Lys	Asn	His	Gly	Cys	Ala	His	Ile	Cys	Arg	Glu	Thr	Pro	
				165					170					175		
Lys	Gly	Gly	Ile	Ala	Cys	Glu	Cys	Arg	Pro	Gly	Phe	Glu	Leu	Thr	Lys	
			180					185					190			
Asn	Gln	Arg	Asp	Cys	Lys	Leu	Thr	Cys	Asn	Tyr	Gly	Asn	Gly	Gly	Cys	
		195					200					205				
Gln	His	Thr	Cys	Asp	Asp	Thr	Glu	Gln	Gly	Pro	Arg	Cys	Gly	Cys	His	
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Ile	Lys	Phe	Val	Leu	His	Thr	Asp	Gly	Lys	Thr	Cys	Ile	Gly	Glu	Arg	
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				245					250					255		
Ala	Val	Asn	Asn	Gly	Gly	Cys	Asp	Ser	Lys	Cys	His	Asp	Ala	Ala	Thr	
			260					265					270			
Gly	Val	His	Cys	Thr	Cys	Pro	Val	Gly	Phe	Met	Leu	Gln	Pro	Asp	Arg	
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Lys	Thr	Cys	Lys	Asp	Ile	Asp	Glu	Cys	Arg	Leu	Asn	Asn	Gly	Gly	Cys	
	290					295					300					
Asp	His	Ile	Cys	Arg	Asn	Thr	Val	Gly	Ser	Phe	Glu	Cys	Ser	Cys	Lys	
305					310					315					320	
Lys	Gly	Tyr	Lys	Leu	Leu	Ile	Asn	Glu	Arg	Asn	Cys	Gln	Asp	Ile	Asp	
				325					330					335		
Glu	Cys	Ser	Phe	Asp	Arg	Thr	Cys	Asp	His	Ile	Cys	Val	Asn	Thr	Pro	
			340					345					350			

Gly Ser Phe Gln Cys Leu Cys His Arg Gly Tyr Leu Leu Tyr Gly Ile
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 Thr His Cys Gly Asp Val Asp Glu Cys Ser Ile Asn Arg Gly Gly Cys
 370 375 380
 Arg Phe Gly Cys Ile Asn Thr Pro Gly Ser Tyr Gln Cys Thr Cys Pro
 385 390 395 400
 Ala Gly Gln Gly Arg Leu His Trp Asn Gly Lys Asp Cys Thr Glu Pro
 405 410 415
 Leu Lys Cys Gln Gly Ser Pro Gly Ala Ser Lys Ala Met Leu Ser Cys
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 Asn Arg Ser Gly Lys Lys Asp Thr Cys Ala Leu Thr Cys Pro Ser Arg
 435 440 445
 Ala Arg Phe Leu Pro Glu Ala Ala Val Leu Ser Ile Lys Gln Arg Ala
 450 455 460
 Ser Phe Lys Ile Lys Asp Ala Lys Cys Arg Leu His Leu Arg Asn Lys
 465 470 475 480
 Gly Lys Thr Glu Glu Ala Gly Arg Thr Thr Gly Pro Gly Gly Ala Pro
 485 490 495
 Cys Ser Glu Cys Gln Val Thr Phe Ile His Leu Lys Cys Asp Ser Ser
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 Arg Lys Gly Lys Gly Arg Arg Ala Arg Thr Pro Pro Gly Lys Glu Val
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 Thr Arg Leu Thr Leu Glu Leu Glu Ala Glu Val Arg Ala Glu Glu Thr
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 Thr Ala Ser Cys Gly Leu Pro Cys Leu Arg Gln Arg Met Glu Arg Arg
 545 550 555 560
 Leu Lys Gly Ser Leu Lys Met Leu Arg Lys Ser Ile Asn Gln Asp Arg
 565 570 575
 Phe Leu Leu Arg Leu Ala Gly Leu Asp Tyr Glu Leu Ala His Lys Pro
 580 585 590
 Gly Leu Val Ala Gly Glu Arg Ala Glu Pro Met Glu Ser Cys Arg Pro
 595 600 605
 Gly Gln His Arg Ala Gly Thr Lys Cys Val Ser Cys Pro Gln Gly Thr
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 Tyr Tyr His Gly Gln Thr Glu Gln Cys Val Pro Cys Pro Ala Gly Thr
 625 630 635 640
 Phe Gln Glu Arg Glu Gly Gln Leu Ser Cys Asp Leu Cys Pro Gly Ser
 645 650 655

Asp	Ala	His	Gly	Pro	Leu	Gly	Ala	Thr	Asn	Val	Thr	Thr	Cys	Ala	Gly	660	665	670
Gln	Cys	Pro	Pro	Gly	Gln	His	Ser	Val	Asp	Gly	Phe	Lys	Pro	Cys	Gln	675	680	685
Pro	Cys	Pro	Arg	Gly	Thr	Tyr	Gln	Pro	Glu	Ala	Gly	Arg	Thr	Leu	Cys	690	695	700
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Arg	Leu	Tyr	Ala	Ser	Glu	Asn	His	Gln	Glu	Ile	Leu	Lys	Asp	Lys	Lys	915	920	925
Leu	Ile	Lys	Ala	Phe	Phe	Glu	Val	Leu	Ala	His	Pro	Gln	Asn	Tyr	Phe	930	935	940
Lys	Tyr	Thr	Glu	Lys	His	Lys	Glu	Met	Leu	Pro	Lys	Ser	Phe	Ile	Lys	945	950	955
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Leu Leu Arg Ser Lys Val Ser Ser Phe Leu Arg Pro Tyr Lys
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<210> 15
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<220>
 <223> Description of Unknown Organism: POLYX
 CG55096-04

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<210> 16

<211> 1009

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX

CG55096-04

<400> 16

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His Ala Arg Ala Ala Gln Tyr Ser Lys Ala Ala Gln Asp Val Asp Glu
      20              25              30

Cys Val Glu Gly Thr Asp Asn Cys His Ile Asp Ala Ile Cys Gln Asn
      35              40              45

Thr Pro Arg Ser Tyr Lys Cys Ile Cys Lys Ser Gly Tyr Thr Gly Asp
      50              55              60

Gly Lys His Cys Lys Asp Val Asp Glu Cys Glu Arg Glu Asp Asn Ala
      65              70              75              80

Gly Cys Val His Asp Cys Val Asn Ile Pro Gly Asn Tyr Arg Cys Thr
      85              90              95

Cys Tyr Asp Gly Phe His Leu Ala His Asp Gly His Asn Cys Leu Asp
      100             105             110

Val Asp Glu Cys Ala Glu Gly Asn Gly Gly Cys Gln Gln Ser Cys Val
      115             120             125

Asn Met Met Gly Ser Tyr Glu Cys His Cys Arg Glu Gly Phe Phe Leu
      130             135             140

Ser Asp Asn Gln His Thr Cys Ile Gln Arg Pro Glu Glu Gly Met Asn
      145             150             155             160

Cys Met Asn Lys Asn His Gly Cys Ala His Ile Cys Arg Glu Thr Pro
      165             170             175

Lys Gly Gly Ile Ala Cys Glu Cys Arg Pro Gly Phe Glu Leu Thr Lys
      180             185             190

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Asn	Gln	Arg	Asp	Cys	Lys	Leu	Thr	Cys	Asn	Tyr	Gly	Asn	Gly	Gly	Cys	
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Gln	His	Thr	Cys	Asp	Asp	Thr	Glu	Gln	Gly	Pro	Arg	Cys	Gly	Cys	His	
		210				215					220					
Ile	Lys	Phe	Val	Leu	His	Thr	Asp	Gly	Lys	Thr	Cys	Ile	Gly	Glu	Arg	
225					230					235					240	
Arg	Leu	Glu	Gln	His	Ile	Pro	Thr	Gln	Ala	Val	Ser	Asn	Glu	Thr	Cys	
				245					250					255		
Ala	Val	Asn	Asn	Gly	Gly	Cys	Asp	Ser	Lys	Cys	His	Asp	Ala	Ala	Thr	
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Gly	Val	His	Cys	Thr	Cys	Pro	Val	Gly	Phe	Met	Leu	Gln	Pro	Asp	Arg	
		275					280					285				
Lys	Thr	Cys	Lys	Asp	Ile	Asp	Glu	Cys	Arg	Leu	Asn	Asn	Gly	Gly	Cys	
	290					295					300					
Asp	His	Ile	Cys	Arg	Asn	Thr	Val	Gly	Ser	Phe	Glu	Cys	Ser	Cys	Lys	
305					310					315					320	
Lys	Gly	Tyr	Lys	Leu	Leu	Ile	Asn	Glu	Arg	Asn	Cys	Gln	Asp	Ile	Asp	
				325					330					335		
Glu	Arg	Ser	Phe	Asp	Arg	Thr	Cys	Asp	His	Ile	Cys	Val	Asn	Thr	Pro	
			340					345					350			
Gly	Ser	Phe	Gln	Cys	Leu	Cys	His	Arg	Gly	Tyr	Leu	Leu	Tyr	Gly	Ile	
		355					360					365				
Thr	His	Cys	Gly	Asp	Val	Asp	Glu	Cys	Ser	Ile	Asn	Arg	Gly	Gly	Cys	
	370					375					380					
Arg	Phe	Gly	Cys	Ile	Asn	Thr	Pro	Gly	Ser	Tyr	Gln	Cys	Thr	Cys	Pro	
385					390					395					400	
Ala	Gly	Gln	Gly	Arg	Leu	His	Trp	Asn	Gly	Lys	Asp	Cys	Thr	Glu	Pro	
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Leu	Lys	Cys	Gln	Gly	Ser	Pro	Gly	Ala	Ser	Lys	Ala	Met	Leu	Ser	Cys	
			420					425					430			
Asn	Arg	Ser	Gly	Lys	Lys	Asp	Thr	Cys	Ala	Leu	Thr	Cys	Pro	Ser	Arg	
		435					440					445				
Ala	Arg	Phe	Leu	Pro	Glu	Ser	Glu	Asn	Gly	Phe	Thr	Val	Ser	Cys	Gly	
	450					455					460					
Thr	Pro	Ser	Pro	Arg	Ala	Ala	Pro	Ala	Arg	Ala	Gly	His	Asn	Gly	Asn	
465					470					475					480	
Ser	Thr	Asn	Ser	Asn	His	Cys	His	Glu	Ala	Ala	Val	Leu	Ser	Ile	Lys	
				485					490					495		

Gln Arg Ala Ser Phe Lys Ile Lys Asp Ala Lys Cys Arg Leu His Leu
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 515 520 525
 Gly Ala Pro Cys Ser Glu Cys Gln Val Thr Phe Ile His Leu Lys Cys
 530 535 540
 Asp Ser Ser Arg Lys Gly Lys Gly Arg Arg Ala Arg Thr Pro Pro Gly
 545 550 555 560
 Lys Glu Val Thr Arg Leu Thr Leu Glu Leu Glu Ala Glu Val Arg Ala
 565 570 575
 Glu Glu Thr Thr Ala Ser Cys Gly Leu Pro Cys Leu Arg Gln Arg Met
 580 585 590
 Glu Arg Arg Leu Lys Gly Ser Leu Lys Met Leu Arg Lys Ser Ile Asn
 595 600 605
 Gln Asp Arg Phe Leu Leu Arg Leu Ala Gly Leu Asp Tyr Glu Leu Ala
 610 615 620
 His Lys Pro Gly Leu Val Ala Gly Glu Arg Ala Glu Pro Met Glu Ser
 625 630 635 640
 Cys Arg Pro Gly Gln His Arg Ala Gly Thr Lys Cys Val Ser Cys Pro
 645 650 655
 Gln Gly Thr Tyr Tyr His Gly Gln Thr Glu Gln Cys Val Pro Cys Pro
 660 665 670
 Ala Gly Thr Phe Gln Glu Arg Glu Gly Gln Leu Ser Cys Asp Leu Cys
 675 680 685
 Pro Gly Ser Asp Ala His Gly Pro Leu Gly Ala Thr Asn Val Thr Thr
 690 695 700
 Cys Ala Gly Gln Cys Pro Pro Gly Gln His Ser Val Asp Gly Phe Lys
 705 710 715 720
 Pro Cys Gln Pro Cys Pro Arg Gly Thr Tyr Gln Pro Glu Ala Gly Arg
 725 730 735
 Thr Leu Cys Phe Pro Cys Gly Gly Gly Leu Thr Thr Lys His Glu Gly
 740 745 750
 Ala Ile Ser Phe Gln Asp Cys Asp Thr Lys Val Gln Cys Ser Pro Gly
 755 760 765
 His Tyr Tyr Asn Thr Ser Ile His Arg Cys Ile Arg Cys Ala Met Gly
 770 775 780
 Ser Tyr Gln Pro Asp Phe Arg Gln Asn Phe Cys Ser Arg Cys Pro Gly
 785 790 795 800

Asn Thr Ser Thr Asp Phe Asp Gly Ser Thr Ser Val Ala Gln Cys Lys
 805 810 815
 Asn Arg Gln Cys Gly Gly Glu Leu Gly Glu Phe Thr Gly Tyr Ile Glu
 820 825 830
 Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala Gly Val Glu Cys Ile Trp
 835 840 845
 Asn Ile Asn Pro Pro Pro Lys Arg Lys Ile Leu Ile Val Val Pro Glu
 850 855 860
 Ile Phe Leu Pro Ser Glu Asp Glu Cys Gly Asp Val Leu Val Met Arg
 865 870 875 880
 Lys Asn Ser Ser Pro Ser Ser Ile Thr Thr Tyr Glu Thr Cys Gln Thr
 885 890 895
 Tyr Glu Arg Pro Ile Ala Phe Thr Ala Arg Ser Arg Lys Leu Trp Ile
 900 905 910
 Asn Phe Lys Thr Ser Glu Ala Asn Ser Ala Arg Gly Phe Gln Ile Pro
 915 920 925
 Tyr Val Thr Tyr Asp Glu Asp Tyr Glu Gln Leu Val Glu Asp Ile Val
 930 935 940
 Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu Ile Leu Lys
 945 950 955 960
 Asp Lys Lys Leu Ile Lys Ala Phe Phe Glu Val Leu Ala His Pro Gln
 965 970 975
 Asn Tyr Phe Lys Tyr Thr Glu Lys His Lys Glu Met Leu Pro Lys Ser
 980 985 990
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<210> 17

<211> 1709

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
10327789.0.16

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 aaaaatagaa tggatctatt ggaaaaacca taaatcatta tttgcttact tcctaattga 360

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<210> 18

<211> 344

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
10327789.0.16

<400> 18

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Ala Gln His Thr Thr Gly Arg Ile Phe Glu Ser Glu Val Arg Tyr Gln
      20             25             30

Cys Asn Pro Gly Tyr Lys Ser Val Gly Ser Pro Val Phe Val Cys Gln
      35             40             45

Ala Asn Arg His Trp His Ser Glu Ser Pro Leu Met Cys Val Pro Leu
      50             55             60

Asp Cys Gly Lys Pro Pro Pro Ile Gln Asn Gly Phe Met Lys Gly Glu
      65             70             75             80

Asn Phe Glu Val Gly Ser Lys Val Gln Phe Phe Cys Asn Glu Gly Tyr
      85             90             95

Glu Leu Val Gly Asp Ser Ser Trp Thr Cys Gln Lys Ser Gly Lys Trp
      100            105            110

Asn Lys Lys Ser Asn Pro Lys Cys Met Pro Ala Lys Cys Pro Glu Pro
      115            120            125

```


Pro Leu Leu Glu Asn Gln Leu Val Leu Lys Glu Leu Thr Thr Glu Val
 130 135 140
 Gly Val Val Thr Phe Ser Cys Lys Glu Gly His Val Leu Gln Gly Pro
 145 150 155 160
 Ser Val Leu Lys Cys Leu Pro Ser Gln Gln Trp Asn Asp Ser Phe Pro
 165 170 175
 Val Cys Lys Ile Val Leu Cys Thr Pro Pro Pro Leu Ile Ser Phe Gly
 180 185 190
 Val Pro Ile Pro Ser Ser Ala Leu His Phe Gly Ser Thr Val Lys Tyr
 195 200 205
 Ser Cys Val Gly Gly Phe Phe Leu Arg Gly Asn Ser Thr Thr Leu Cys
 210 215 220
 Gln Pro Asp Gly Thr Trp Ser Ser Pro Leu Pro Glu Cys Val Pro Val
 225 230 235 240
 Glu Cys Pro Gln Pro Glu Glu Ile Pro Asn Gly Ile Ile Asp Val Gln
 245 250 255
 Gly Leu Ala Tyr Leu Ser Thr Ala Leu Tyr Thr Cys Lys Pro Gly Phe
 260 265 270
 Glu Leu Val Gly Asn Thr Thr Thr Leu Cys Gly Glu Asn Gly His Trp
 275 280 285
 Leu Gly Gly Lys Pro Thr Cys Lys Ala Ile Glu Cys Leu Lys Pro Lys
 290 295 300
 Glu Ile Leu Asn Gly Lys Phe Ser Tyr Thr Asp Leu His Tyr Gly Gln
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<210> 19

<211> 1952

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX

10327789.0.140

<400> 19

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<210> 20

<211> 406

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
10327789.0.140

<400> 20

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```

Met Asn Gly Tyr Ala Ser Gly Ser Asn Tyr Ser Phe Gly Ala Met Val
      20               25               30

```

```

Ala Tyr Ser Cys Asn Lys Gly Phe Tyr Ile Lys Gly Glu Lys Lys Ser
  35               40               45

```

```

Thr Cys Glu Ala Thr Gly Gln Trp Ser Ser Pro Ile Pro Thr Cys His
  50               55               60

```

```

Pro Val Ser Cys Gly Glu Pro Pro Lys Val Glu Asn Gly Phe Leu Glu
  65               70               75               80

```

```

His Thr Thr Gly Arg Ile Phe Glu Ser Glu Val Arg Tyr Gln Cys Asn
  85               90               95

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Pro Gly Tyr Lys Ser Val Gly Ser Pro Val Phe Val Cys Gln Ala Asn	100	105	110
Arg His Trp His Ser Glu Ser Pro Leu Met Cys Val Pro Leu Asp Cys	115	120	125
Gly Lys Pro Pro Pro Ile Gln Asn Gly Phe Met Lys Gly Glu Asn Phe	130	135	140
Glu Val Gly Ser Lys Val Gln Phe Phe Cys Asn Glu Gly Tyr Glu Leu	145	150	155
Val Gly Asp Ser Ser Trp Thr Cys Gln Lys Ser Gly Lys Trp Asn Lys	165	170	175
Lys Ser Asn Pro Lys Cys Met Pro Ala Lys Cys Pro Glu Pro Pro Leu	180	185	190
Leu Glu Asn Gln Leu Val Leu Lys Glu Leu Thr Thr Glu Val Gly Val	195	200	205
Val Thr Phe Ser Cys Lys Glu Gly His Val Leu Gln Gly Pro Ser Val	210	215	220
Leu Lys Cys Leu Pro Ser Gln Gln Trp Asn Asp Ser Phe Pro Val Cys	225	230	235
Lys Ile Val Leu Cys Thr Pro Pro Pro Leu Ile Ser Phe Gly Val Pro	245	250	255
Ile Pro Ser Ser Ala Leu His Phe Gly Ser Thr Val Lys Tyr Ser Cys	260	265	270
Val Gly Gly Phe Phe Leu Arg Gly Asn Ser Thr Thr Leu Cys Gln Pro	275	280	285
Asp Gly Thr Trp Ser Ser Pro Leu Pro Glu Cys Val Pro Val Glu Cys	290	295	300
Pro Gln Pro Glu Glu Ile Pro Asn Gly Ile Ile Asp Val Gln Gly Leu	305	310	315
Ala Tyr Leu Ser Thr Ala Leu Tyr Thr Cys Lys Pro Gly Phe Glu Leu	325	330	335
Val Gly Asn Thr Thr Thr Leu Cys Gly Glu Asn Gly His Trp Leu Gly	340	345	350
Gly Lys Pro Thr Cys Lys Ala Ile Glu Cys Leu Lys Pro Lys Glu Ile	355	360	365
Leu Asn Gly Lys Phe Ser Tyr Thr Asp Leu His Tyr Gly Gln Thr Val	370	375	380
Thr Tyr Ser Cys Asn Arg Gly Phe Arg Leu Glu Gly Ser Gln Cys Leu	385	390	395
			400

Asp Leu Phe Arg Asp Arg
405

<210> 21
<211> 6153
<212> DNA
<213> Unknown Organism

<220>
<221> modified_base
<222> (1010)
<223> a, c, t, g, other or unknown

<220>
<223> Description of Unknown Organism: POLYX
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Tyr Thr Leu Ala Gly Leu Asp Thr Ile Glu Cys Leu Ala Asp Gly Lys
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Trp Ser Arg Ser Asp Gln Gln Cys Leu Ala Val Ser Cys Asp Glu Pro
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Pro Ile Val Asp His Ala Ser Pro Glu Thr Ala His Arg Leu Phe Gly
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Gln Asp Met Pro Arg Cys Ile Ala His Phe Cys Glu Lys Pro Pro Ser
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Cys	Lys	Ile	Val	Leu	Cys	Thr	Pro	Pro	Pro	Leu	Ile	Ser	Phe	Gly	Val	450	455	460
Pro	Ile	Pro	Ser	Ser	Ala	Leu	His	Phe	Gly	Ser	Thr	Val	Lys	Tyr	Ser	465	470	475
Cys	Val	Gly	Gly	Phe	Phe	Leu	Arg	Gly	Asn	Ser	Thr	Thr	Leu	Cys	Gln	485	490	495

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 1940 1945 1950
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Ala Lys
 2050

<210> 23

<211> 2216

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
 AC016030_A.0.82

<400> 23

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cattgcctga cgatactgta attgagagt aagcactgcc cagtgatatt gcagccgagg 2040
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gctgggtgaag ggccttcttc cctgatcagg gagaaacctg ttcccaaaca gaatgggaat 2160
gaagaggaaa atctttgata agagcagact ggaagtctaa aacaggagtt ggatga 2216

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<210> 24
 <211> 457
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: POLYX
 AC016030_A.0.82

<400> 24
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 1 5 10 15
 Pro Ser Gly Val Val Leu Cys Leu Leu Gly Ala Cys Phe Gln Met Leu
 20 25 30
 Pro Ala Ala Pro Ser Gly Cys Pro Gln Leu Cys Arg Cys Glu Gly Arg
 35 40 45
 Leu Leu Tyr Cys Glu Ala Leu Asn Leu Thr Glu Ala Pro His Asn Leu
 50 55 60
 Ser Gly Leu Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Ser Glu Leu
 65 70 75 80
 Arg Ala Gly Gln Phe Thr Gly Leu Met Gln Leu Thr Trp Leu Tyr Leu
 85 90 95
 Asp His Asn His Ile Cys Ser Val Gln Gly Asp Ala Phe Gln Lys Leu
 100 105 110
 Arg Arg Val Lys Glu Leu Thr Leu Ser Ala Tyr Arg Ser Cys Gly Gly
 115 120 125
 Val Ser Thr Arg Asn His Glu Val Glu Gly His Lys Ile Lys Ala Lys
 130 135 140
 Ala Val Lys Leu Trp Gln Ile Ser Asp Lys Gly Asn Gln Ser Cys Gly
 145 150 155 160
 Lys Met Glu Gly Asn Gly Gln Met Asp Asp Leu Val Cys Phe Glu Glu
 165 170 175
 Leu Thr Asp Tyr Gln Leu Val Ser Pro Ala Lys Asn Pro Ser Ser Leu
 180 185 190
 Phe Ser Lys Glu Ala Pro Lys Arg Lys Ala Gln Ala Val Ser Glu Glu
 195 200 205
 Glu Glu Glu Glu Glu Gly Lys Ser Ser Ser Pro Lys Lys Lys Ile Lys
 210 215 220
 Leu Lys Lys Ser Lys Asn Val Ala Thr Glu Gly Thr Ser Thr Gln Lys
 225 230 235 240
 Glu Phe Glu Val Lys Asp Pro Glu Leu Glu Ala Gln Gly Asp Asp Met
 245 250 255

Val Cys Asp Asp Pro Glu Ala Gly Glu Met Thr Ser Glu Asn Leu Val
 260 265 270

Gln Thr Ala Pro Lys Lys Lys Lys Asn Lys Gly Lys Lys Gly Leu Glu
 275 280 285

Pro Ser Gln Ser Thr Ala Ala Lys Val Pro Lys Lys Ala Lys Thr Trp
 290 295 300

Ile Pro Glu Val His Asp Gln Lys Ala Asp Val Ser Ala Trp Lys Asp
 305 310 315 320

Leu Phe Val Pro Arg Pro Val Leu Arg Ala Leu Ser Phe Leu Gly Phe
 325 330 335

Ser Ala Pro Thr Pro Ile Gln Ala Leu Thr Leu Ala Pro Ala Ile Arg
 340 345 350

Asp Lys Leu Asp Ile Leu Gly Ala Ala Glu Thr Gly Ser Gly Lys Thr
 355 360 365

Leu Ala Phe Ala Ile Pro Met Ile His Ala Val Leu Gln Trp Gln Lys
 370 375 380

Arg Asn Ala Ala Pro Pro Pro Ser Asn Thr Glu Ala Pro Pro Gly Glu
 385 390 395 400

Thr Arg Thr Glu Ala Gly Ala Glu Thr Arg Leu Pro Gly Lys Ala Glu
 405 410 415

Ala Glu Ser Asp Ala Leu Pro Asp Asp Thr Val Ile Glu Ser Glu Ala
 420 425 430

Leu Pro Ser Asp Ile Ala Ala Glu Ala Arg Ala Lys Thr Gly Gly Thr
 435 440 445

Val Ser Asp Gln Ala Leu Leu Phe Glu
 450 455

<210> 25

<211> 921

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
 h_nh0443k08_A

<400> 25

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 aatttccaag ccaagcctga tgatcttatt ctggcaactt acccaaagtc aggtacaaca 180
 tggatgcatg aaattttaga catgattcta aatgatggtg atgtggagaa atgcaaaaga 240
 gccagactc tagatagaca cgctttcctt gaactgaaat ttcccataa agaaaaacca 300
 gatttggagt tcgttcttga aatgtcctca ccacaactga taaaaacaca tctcccttca 360
 catctgattc caccatctat ctggaaagaa aactgcaaga ttgtctatgt ggccagaaat 420

```

cccaaggatt gcctggtgtc ctactaccac tttcacagga tggcttcctt tatgcctgat 480
cctcagaact tagaggaatt ttatgagaaa ttcattgtccg gaaaagggtga gttcgggtcc 540
tggtttgacc atgtgaaagg atggtgggct gcaaaaagaca tgcaccggat cctctacctc 600
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gagaaaaactt ggtcagggtga tgttataaac aagattgtcc accatacctc atttgatgta 720
atgaaggata atcccatggc caaccatact gcggtacctg ctcacatatt caatcactcc 780
atctcaaaat ttatgaggaa aggtgggatg cctggagact ggaagaacca ctttactgtg 840
gctttgaatg agaactttga taagcattat gaaaagaaga tggcagggtc cacactgaac 900
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<210> 26

<211> 305

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX

h_nh0443k08_A

<400> 26

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Met Ala Lys Ile Glu Lys Asn Ala Pro Thr Met Glu Lys Lys Pro Glu
 1             5             10             15

```

```

Leu Phe Asn Ile Met Glu Val Asp Gly Val Pro Thr Leu Ile Leu Ser
          20             25             30

```

```

Lys Glu Trp Trp Glu Lys Val Cys Asn Phe Gln Ala Lys Pro Asp Asp
          35             40             45

```

```

Leu Ile Leu Ala Thr Tyr Pro Lys Ser Gly Thr Thr Trp Met His Glu
 50             55             60

```

```

Ile Leu Asp Met Ile Leu Asn Asp Gly Asp Val Glu Lys Cys Lys Arg
 65             70             75             80

```

```

Ala Gln Thr Leu Asp Arg His Ala Phe Leu Glu Leu Lys Phe Pro His
          85             90             95

```

```

Lys Glu Lys Pro Asp Leu Glu Phe Val Leu Glu Met Ser Ser Pro Gln
          100            105            110

```

```

Leu Ile Lys Thr His Leu Pro Ser His Leu Ile Pro Pro Ser Ile Trp
          115            120            125

```

```

Lys Glu Asn Cys Lys Ile Val Tyr Val Ala Arg Asn Pro Lys Asp Cys
          130            135            140

```

```

Leu Val Ser Tyr Tyr His Phe His Arg Met Ala Ser Phe Met Pro Asp
          145            150            155            160

```

```

Pro Gln Asn Leu Glu Glu Phe Tyr Glu Lys Phe Met Ser Gly Lys Gly
          165            170            175

```

```

Glu Phe Gly Ser Trp Phe Asp His Val Lys Gly Trp Trp Ala Ala Lys
          180            185            190

```


Asp Met His Arg Ile Leu Tyr Leu Phe Tyr Glu Asp Ile Lys Gln Asn
195 200 205

Pro Lys His Glu Ile His Lys Val Leu Glu Phe Leu Glu Lys Thr Trp
210 215 220

Ser Gly Asp Val Ile Asn Lys Ile Val His His Thr Ser Phe Asp Val
225 230 235 240

Met Lys Asp Asn Pro Met Ala Asn His Thr Ala Val Pro Ala His Ile
245 250 255

Phe Asn His Ser Ile Ser Lys Phe Met Arg Lys Gly Gly Met Pro Gly
260 265 270

Asp Trp Lys Asn His Phe Thr Val Ala Leu Asn Glu Asn Phe Asp Lys
275 280 285

His Tyr Glu Lys Lys Met Ala Gly Ser Thr Leu Asn Phe Cys Leu Glu
290 295 300

Ile
305

<210> 27

<211> 893

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
h_nh0778p17_A

<400> 27

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tatttatgaa agagagcctg tagctgagag acacctacat gaaatccaaa aactacagga 180
aagtattaac aatttggcag ataatgttca aaaatttggg cagcaacaga aaagtctggt 240
ggcttcaatg agaaggttta gtctacttaa gagagagtct accattacaa aggagataaa 300
aattcaggca gaatacatca acagaagttt gaatgattta gttaaagaag ttaaaaagtc 360
agaggttgaa aatggtccat cttcagtggg cacaaggata cttaaattctc agcatgctgc 420
aatgttccgc cattttcagc aaatcatgtt tatatacaat gacacaatag cagcaaagca 480
agagaagtgc aagacattta ttttacgtca gcttgaagtt gctggaaaag agatgtctga 540
agaagatgta aatgatatgc ttcacatcagg aaaatgggaa gtttttaattg aaagcttact 600
tacagaaatc aatatcacta aagcacaact ttcagagatt gaacagagac acaaggaact 660
tgtaatttg gagaaccaa taaaggattt aagggatctt ttcattcaga tatctctttt 720
agtagaggaa caaggagaga gcatcaacaa tattgaaatg acagtgaata gtacaaaaga 780
gtatgttaac aatactaaag agaaatttgg actagctgta aaatacaaaa aaagaaatcc 840
ttgcagagta ctgtgtgtgt ggtgctgtcc atgctgtagc tcaaaataaa gaa 893

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<210> 28

<211> 294

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
h_nh0778p17_A

<400> 28

Met	Lys	Asp	Arg	Leu	Gln	Glu	Leu	Lys	Gln	Arg	Thr	Lys	Glu	Ile	Glu	1	5	10	15
Leu	Ser	Arg	Asp	Ser	His	Val	Ser	Thr	Thr	Glu	Thr	Glu	Glu	Gln	Gly	20	25	30	
Val	Phe	Leu	Gln	Gln	Ala	Val	Ile	Tyr	Glu	Arg	Glu	Pro	Val	Ala	Glu	35	40	45	
Arg	His	Leu	His	Glu	Ile	Gln	Lys	Leu	Gln	Glu	Ser	Ile	Asn	Asn	Leu	50	55	60	
Ala	Asp	Asn	Val	Gln	Lys	Phe	Gly	Gln	Gln	Gln	Lys	Ser	Leu	Val	Ala	65	70	75	80
Ser	Met	Arg	Arg	Phe	Ser	Leu	Leu	Lys	Arg	Glu	Ser	Thr	Ile	Thr	Lys	85	90	95	
Glu	Ile	Lys	Ile	Gln	Ala	Glu	Tyr	Ile	Asn	Arg	Ser	Leu	Asn	Asp	Leu	100	105	110	
Val	Lys	Glu	Val	Lys	Lys	Ser	Glu	Val	Glu	Asn	Gly	Pro	Ser	Ser	Val	115	120	125	
Val	Thr	Arg	Ile	Leu	Lys	Ser	Gln	His	Ala	Ala	Met	Phe	Arg	His	Phe	130	135	140	
Gln	Gln	Ile	Met	Phe	Ile	Tyr	Asn	Asp	Thr	Ile	Ala	Ala	Lys	Gln	Glu	145	150	155	160
Lys	Cys	Lys	Thr	Phe	Ile	Leu	Arg	Gln	Leu	Glu	Val	Ala	Gly	Lys	Glu	165	170	175	
Met	Ser	Glu	Glu	Asp	Val	Asn	Asp	Met	Leu	His	Gln	Gly	Lys	Trp	Glu	180	185	190	
Val	Phe	Asn	Glu	Ser	Leu	Leu	Thr	Glu	Ile	Asn	Ile	Thr	Lys	Ala	Gln	195	200	205	
Leu	Ser	Glu	Ile	Glu	Gln	Arg	His	Lys	Glu	Leu	Val	Asn	Leu	Glu	Asn	210	215	220	
Gln	Ile	Lys	Asp	Leu	Arg	Asp	Leu	Phe	Ile	Gln	Ile	Ser	Leu	Leu	Val	225	230	235	240
Glu	Glu	Gln	Gly	Glu	Ser	Ile	Asn	Asn	Ile	Glu	Met	Thr	Val	Asn	Ser	245	250	255	
Thr	Lys	Glu	Tyr	Val	Asn	Asn	Thr	Lys	Glu	Lys	Phe	Gly	Leu	Ala	Val	260	265	270	
Lys	Tyr	Lys	Lys	Arg	Asn	Pro	Cys	Arg	Val	Leu	Cys	Cys	Trp	Cys	Cys	275	280	285	

Pro Cys Cys Ser Ser Lys
290

<210> 29
<211> 892
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: POLYX
hnh0778p17_A1

<400> 29
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atztatgaaa gagagcctgt agctgagaga cacctacatg aaatccaaaa actacaggaa 180
agtattaaca atttggcaga taatgttcaa aaatttgggc agcaacagaa aagtcctggtg 240
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gaggttgaaa atggtccatc ttcagtgggc acaaggatac ttaaattctca gcatgctgca 420
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gagaagtgca agacatttat tttacgtcag cttgaagttg ctggaaaaga gatgtctgaa 540
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gttaatttgg agaaccaaat aaaggattta agggatcttt tcattcagat atctctttta 720
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tgcagagtac tgtgtgtgtg gtgctgtcca tgctgtagct caaaataaag aa 892

<210> 30
<211> 294
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: POLYX
hnh0778p17_A1

<400> 30
Met Lys Asp Arg Leu Gln Glu Leu Lys Gln Arg Thr Lys Glu Ile Glu
1 5 10 15
Leu Ser Arg Asp Ser His Val Ser Thr Thr Glu Thr Glu Glu Gln Gly
20 25 30
Val Phe Leu Gln Gln Ala Val Ile Tyr Glu Arg Glu Pro Val Ala Glu
35 40 45
Arg His Leu His Glu Ile Gln Lys Leu Gln Glu Ser Ile Asn Asn Leu
50 55 60
Ala Asp Asn Val Gln Lys Phe Gly Gln Gln Gln Lys Ser Leu Val Ala
65 70 75 80

Ser Met Arg Arg Phe Ser Leu Leu Lys Arg Glu Ser Thr Ile Thr Lys
 85 90 95
 Glu Ile Lys Ile Gln Ala Glu Tyr Ile Asn Arg Ser Leu Asn Asp Leu
 100 105 110
 Val Lys Glu Val Lys Lys Ser Glu Val Glu Asn Gly Pro Ser Ser Val
 115 120 125
 Val Thr Arg Ile Leu Lys Ser Gln His Ala Ala Met Phe Arg His Phe
 130 135 140
 Gln Gln Ile Met Phe Ile Tyr Asn Asp Thr Ile Ala Ala Lys Gln Glu
 145 150 155 160
 Lys Cys Lys Thr Phe Ile Leu Arg Gln Leu Glu Val Ala Gly Lys Glu
 165 170 175
 Met Ser Glu Glu Asp Val Asn Asp Met Leu His Gln Gly Lys Trp Glu
 180 185 190
 Val Phe Asn Glu Ser Leu Leu Thr Glu Ile Asn Ile Thr Lys Ala Gln
 195 200 205
 Leu Ser Glu Ile Glu Gln Arg His Lys Glu Leu Val Asn Leu Glu Asn
 210 215 220
 Gln Ile Lys Asp Leu Arg Asp Leu Phe Ile Gln Ile Ser Leu Leu Val
 225 230 235 240
 Glu Glu Gln Gly Glu Ser Ile Asn Asn Ile Glu Met Thr Val Asn Ser
 245 250 255
 Thr Lys Glu Tyr Val Asn Asn Thr Lys Glu Lys Phe Gly Leu Ala Val
 260 265 270
 Lys Tyr Lys Lys Arg Asn Pro Cys Arg Val Leu Cys Cys Trp Cys Cys
 275 280 285
 Pro Cys Cys Ser Ser Lys
 290

<210> 31

<211> 892

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
CG55655_02

<400> 31

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 atttatgaaa gagagcctgt agctgagaga cacctacatg aaatccaaaa actacaggaa 180
 agtattaaca atttggcaga taatgttcaa aaatttgggc agcaacagaa aagtctggtg 240
 gcttcaatga gaaggtttag tctacttaag agagagtcta ccattacaaa ggagataaaa 300

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attcaggcag aatacatcaa cagaagtttg aatgatttag ttaaagaagt taaaaagtca 360
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atgttccgcc atttttcagca aatcatgttt atatacaatg acacaatagc agcaaagcaa 480
gagaagtgcag agacatttat ttacgtcag cttgaagttg ctggaaaaga gatgtctgaa 540
gaagatgtaa atgatatgct tcatcaagga aaatgggaag tttttaatga aagcttactt 600
acagaaatca atatcactaa agcacaactt tcagagattg aacagagaca caaggaactt 660
gttaatttgg agaaccacaaat aaaggattta agggatcttt tcattcagat atctctttta 720
gtagaggaac aaggagagag catcaacaat attgaaatga cagtgaatag tacaaaagag 780
tatgttaaca atactaaaga gaaatttgga ctagctgtaa aatacaaaaa aagaaatcct 840
tgcagagtac tgtgttggtg gtgctgtcca tgctgtagct caaaataaag aa 892

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<210> 32

<211> 294

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
CG55655_02

<400> 32

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Met Lys Asp Arg Leu Gln Glu Leu Lys Gln Arg Thr Lys Glu Ile Glu
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Leu Ser Arg Asp Ser His Val Ser Thr Thr Glu Thr Glu Glu Gln Gly
                20                      25                      30

Val Phe Leu Gln Gln Ala Val Ile Tyr Glu Arg Glu Pro Val Ala Glu
    35                      40                      45

Arg His Leu His Glu Ile Gln Lys Leu Gln Glu Ser Ile Asn Asn Leu
    50                      55                      60

Ala Asp Asn Val Gln Lys Phe Gly Gln Gln Gln Lys Ser Leu Val Ala
    65                      70                      75                      80

Ser Met Arg Arg Phe Ser Leu Leu Lys Arg Glu Ser Thr Ile Thr Lys
                85                      90                      95

Glu Ile Lys Ile Gln Ala Glu Tyr Ile Asn Arg Ser Leu Asn Asp Leu
    100                      105                      110

Val Lys Glu Val Lys Lys Ser Glu Val Glu Asn Gly Pro Ser Ser Val
    115                      120                      125

Val Thr Arg Ile Leu Lys Ser Gln His Ala Ala Met Phe Arg His Phe
    130                      135                      140

Gln Gln Ile Met Phe Ile Tyr Asn Asp Thr Ile Ala Ala Lys Gln Glu
    145                      150                      155                      160

Lys Cys Lys Thr Phe Ile Leu Arg Gln Leu Glu Val Ala Gly Lys Glu
                165                      170                      175

Met Ser Glu Glu Asp Val Asn Asp Met Leu His Gln Gly Lys Trp Glu
    180                      185                      190

```

Val Phe Asn Glu Ser Leu Leu Thr Glu Ile Asn Ile Thr Lys Ala Gln
 195 200 205

Leu Ser Glu Ile Glu Gln Arg His Lys Glu Leu Val Asn Leu Glu Asn
 210 215 220

Gln Ile Lys Asp Leu Arg Asp Leu Phe Ile Gln Ile Ser Leu Leu Val
 225 230 235 240

Glu Glu Gln Gly Glu Ser Ile Asn Asn Ile Glu Met Thr Val Asn Ser
 245 250 255

Thr Lys Glu Tyr Val Asn Asn Thr Lys Glu Lys Phe Gly Leu Ala Val
 260 265 270

Lys Tyr Lys Lys Arg Asn Pro Cys Arg Val Leu Cys Cys Trp Cys Cys
 275 280 285

Pro Cys Cys Ser Ser Lys
 290

<210> 33
 <211> 967
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: POLYX
 GM_11817402_A

<400> 33
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 gaggtgtggg gaactctgcc ttctacaatg tgatgctgca cagagagctg tctgtcatct 180
 tcgaccaatt ccatggcatt caggacactg tgatagggga aggaacgcac tttctcatcc 240
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 tcaactgtgag caaagattgt caccatgtca ccatcacact gggcgctctc tccccgcctt 360
 gttgctggcc aggtccttgc atcttccaat tactggagaa gccaatgaag aatgtgctgc 420
 catccatcac tgcggagctc ctcaagctgg gggcggtca ggctgacgt ggagaactga 480
 tcacgcaggg agagctgggc tccagacagg tgagcgagca attaaactgag caagcagcaa 540
 cctttgggtt cctcctggat gctgtgacct tggatctgac cttcgggaag gaatttgcag 600
 aagcagtggg accaaaggag gtggctcagc aggaagaaga gagggccaga tctgtggtgg 660
 caagggctga gcagcagaag acggcggccca tcatctctgc cgagggcgac tccaaggcca 720
 cggagtcat cgccagctca gtggccaccg caggtgacgg cctgatcaag gccacacaagc 780
 tggaaccatg gaggacactg gccctccagc tctcagaact catccacctc atccacctgc 840
 ccgtggggac atctgtgctc ctccagctgc cccagcgag gccgccctga cctgcacctc 900
 ctccagccaa ctggggccaca gcaccaatga cttttactac cgccttcctt ctgtcccccac 960
 tccagaa 967

<210> 34
 <211> 271
 <212> PRT
 <213> Unknown Organism

<220>

<223> Description of Unknown Organism: POLYX
GM_11817402_A

<400> 34

Met	Glu	Thr	Gln	Leu	Pro	Ser	Leu	Pro	Leu	Ser	Leu	Ala	Ser	Ala	Gly	1	5	10	15
Gly	Val	Gly	Asn	Ser	Ala	Phe	Tyr	Asn	Val	Met	Leu	His	Arg	Glu	Leu	20	25	30	
Ser	Val	Ile	Phe	Asp	Gln	Phe	His	Gly	Ile	Gln	Asp	Thr	Val	Ile	Gly	35	40	45	
Glu	Gly	Thr	His	Phe	Leu	Ile	Pro	Trp	Glu	Lys	Lys	Pro	Ile	Ile	Phe	50	55	60	
Asp	Cys	Cys	Ser	Arg	Pro	His	Tyr	Ala	Pro	Ile	Ile	Thr	Val	Ser	Lys	65	70	75	80
Asp	Cys	His	His	Val	Thr	Ile	Thr	Leu	Gly	Val	Leu	Phe	Pro	Pro	Cys	85	90	95	
Cys	Trp	Pro	Gly	Pro	Cys	Ile	Phe	Gln	Leu	Leu	Glu	Lys	Pro	Met	Lys	100	105	110	
Asn	Val	Leu	Pro	Ser	Ile	Thr	Ala	Glu	Leu	Leu	Lys	Leu	Gly	Ala	Ala	115	120	125	
Gln	Ala	Asp	Ala	Gly	Glu	Leu	Ile	Thr	Gln	Gly	Glu	Leu	Gly	Ser	Arg	130	135	140	
Gln	Val	Ser	Glu	Gln	Leu	Thr	Glu	Gln	Ala	Ala	Thr	Phe	Gly	Phe	Leu	145	150	155	160
Leu	Asp	Ala	Val	Thr	Leu	Asp	Leu	Thr	Phe	Gly	Lys	Glu	Phe	Ala	Glu	165	170	175	
Ala	Val	Glu	Pro	Lys	Glu	Val	Ala	Gln	Gln	Glu	Glu	Glu	Arg	Ala	Arg	180	185	190	
Ser	Val	Val	Ala	Arg	Ala	Glu	Gln	Gln	Lys	Thr	Ala	Ala	Ile	Ile	Ser	195	200	205	
Ala	Glu	Gly	Asp	Ser	Lys	Ala	Thr	Glu	Phe	Ile	Ala	Ser	Ser	Val	Ala	210	215	220	
Thr	Ala	Gly	Asp	Gly	Leu	Ile	Lys	Ala	His	Lys	Leu	Glu	Pro	Trp	Arg	225	230	235	240
Thr	Leu	Ala	Leu	Gln	Leu	Ser	Glu	Leu	Ile	His	Leu	Ile	His	Leu	Pro	245	250	255	
Val	Gly	Thr	Ser	Val	Leu	Leu	Gln	Leu	Pro	Gln	Arg	Arg	Pro	Pro	260	265	270		

<210> 35
 <211> 464
 <212> PRT
 <213> Rattus norvegicus

<400> 35
 Met Val Leu Ala Phe Trp Leu Ala Phe Phe Thr Tyr Thr Trp Ile Thr
 1 5 10 15
 Leu Met Leu Asp Ala Ser Ala Val Lys Glu Pro His Gln Gln Cys Leu
 20 25 30
 Ser Ser Pro Lys Gln Thr Arg Ile Arg Glu Thr Arg Met Arg Lys Asp
 35 40 45
 Asp Leu Thr Lys Val Trp Pro Leu Lys Arg Glu Gln Leu Leu His Ile
 50 55 60
 Glu Asp His Asp Phe Ser Thr Arg Pro Gly Phe Gly Gly Ser Pro Val
 65 70 75 80
 Pro Val Gly Ile Asp Val Gln Val Glu Ser Ile Asp Ser Ile Ser Glu
 85 90 95
 Val Asn Met Asp Phe Thr Met Thr Phe Tyr Leu Arg His Tyr Trp Lys
 100 105 110
 Asp Glu Arg Leu Ser Phe Pro Ser Thr Thr Asn Lys Ser Met Thr Phe
 115 120 125
 Asp Arg Arg Leu Ile Gln Lys Ile Trp Val Pro Asp Ile Phe Phe Val
 130 135 140
 His Ser Lys Arg Ser Phe Ile His Asp Thr Thr Val Glu Asn Ile Met
 145 150 155 160
 Leu Arg Val His Pro Asp Gly Asn Val Leu Phe Ser Leu Arg Ile Thr
 165 170 175
 Val Ser Ala Met Cys Phe Met Asp Phe Ser Arg Phe Pro Leu Asp Thr
 180 185 190
 Gln Asn Cys Ser Leu Glu Leu Glu Ser Tyr Ala Tyr Asn Glu Glu Asp
 195 200 205
 Leu Met Leu Tyr Trp Lys His Gly Asn Lys Ser Leu Asn Thr Glu Glu
 210 215 220
 His Ile Ser Leu Ser Gln Phe Phe Ile Glu Glu Phe Ser Ala Ser Ser
 225 230 235 240
 Gly Leu Ala Phe Tyr Ser Ser Thr Gly Trp Tyr Tyr Arg Leu Phe Ile
 245 250 255
 Asn Phe Val Leu Arg Arg His Ile Phe Phe Phe Val Leu Gln Thr Tyr
 260 265 270

Phe Pro Ala Met Leu Met Val Met Leu Ser Trp Val Ser Phe Trp Ile
 275 280 285
 Asp Arg Arg Ala Val Pro Ala Arg Val Ser Leu Gly Ile Thr Thr Val
 290 295 300
 Leu Thr Met Ser Thr Ile Val Thr Gly Val Ser Ala Ser Met Pro Gln
 305 310 315 320
 Val Ser Tyr Val Lys Ala Val Asp Val Tyr Met Trp Val Ser Ser Leu
 325 330 335
 Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn Tyr Leu Thr
 340 345 350
 Thr Val Glu Glu Trp Lys Gln Leu Asn Arg Arg Gly Lys Ile Ser Gly
 355 360 365
 Met Tyr Asn Ile Asp Ala Val Gln Ala Met Ala Phe Asp Gly Cys Tyr
 370 375 380
 His Asp Gly Glu Thr Asp Val Asp Gln Thr Ser Phe Phe Leu His Ser
 385 390 395 400
 Glu Glu Asp Ser Met Arg Thr Lys Phe Thr Gly Ser Pro Cys Ala Asp
 405 410 415
 Ser Ser Gln Ile Lys Arg Lys Ser Leu Gly Gly Asn Val Gly Arg Ile
 420 425 430
 Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg Ile Val Phe
 435 440 445
 Pro Val Val Tyr Ile Ile Phe Asn Leu Phe Tyr Trp Gly Ile Tyr Val
 450 455 460

<210> 36

<211> 464

<212> PRT

<213> Rattus norvegicus

<400> 36

Met Val Leu Ala Phe Trp Leu Ala Phe Phe Thr Tyr Thr Trp Ile Thr
 1 5 10 15
 Leu Met Leu Asp Ala Ser Ala Val Lys Glu Pro His Gln Gln Cys Leu
 20 25 30
 Ser Ser Pro Lys Gln Thr Arg Ile Arg Glu Thr Arg Met Arg Lys Asp
 35 40 45
 Asp Leu Thr Lys Val Trp Pro Leu Lys Arg Glu Gln Leu Leu His Ile
 50 55 60
 Glu Asp His Asp Phe Ser Thr Arg Pro Gly Phe Gly Gly Ser Pro Val
 65 70 75 80

Pro	Val	Gly	Ile	Asp	Val	Gln	Val	Glu	Ser	Ile	Asp	Ser	Ile	Ser	Glu	85	90	95
Val	Asn	Met	Asp	Phe	Thr	Met	Thr	Phe	Tyr	Leu	Arg	His	Tyr	Trp	Lys	100	105	110
Asp	Glu	Arg	Leu	Ser	Phe	Pro	Ser	Thr	Thr	Asn	Lys	Ser	Met	Thr	Phe	115	120	125
Asp	Arg	Arg	Leu	Ile	Gln	Lys	Ile	Trp	Val	Pro	Asp	Ile	Phe	Phe	Val	130	135	140
His	Ser	Lys	Arg	Ser	Phe	Ile	His	Asp	Thr	Thr	Val	Glu	Asn	Ile	Met	145	150	155
Leu	Arg	Val	His	Pro	Asp	Gly	Asn	Val	Leu	Phe	Ser	Leu	Arg	Ile	Thr	165	170	175
Val	Ser	Ala	Met	Cys	Phe	Met	Asp	Phe	Ser	Arg	Phe	Pro	Leu	Asp	Thr	180	185	190
Gln	Asn	Cys	Ser	Leu	Glu	Leu	Glu	Ser	Tyr	Ala	Tyr	Asn	Glu	Glu	Asp	195	200	205
Leu	Met	Leu	Tyr	Trp	Lys	His	Gly	Asn	Lys	Ser	Leu	Asn	Thr	Glu	Glu	210	215	220
His	Ile	Ser	Leu	Ser	Gln	Phe	Phe	Ile	Glu	Glu	Phe	Ser	Ala	Ser	Ser	225	230	235
Gly	Leu	Ala	Phe	Tyr	Ser	Ser	Thr	Gly	Trp	Tyr	Tyr	Arg	Leu	Phe	Ile	245	250	255
Asn	Phe	Val	Leu	Arg	Arg	His	Ile	Phe	Phe	Phe	Val	Leu	Gln	Thr	Tyr	260	265	270
Phe	Pro	Ala	Met	Leu	Met	Val	Met	Leu	Ser	Trp	Val	Ser	Phe	Trp	Ile	275	280	285
Asp	Arg	Arg	Ala	Val	Pro	Ala	Arg	Val	Ser	Leu	Gly	Ile	Thr	Thr	Val	290	295	300
Leu	Thr	Met	Ser	Thr	Ile	Val	Thr	Gly	Val	Ser	Ala	Ser	Met	Pro	Gln	305	310	315
Val	Ser	Tyr	Val	Lys	Ala	Val	Asp	Val	Tyr	Met	Trp	Val	Ser	Ser	Leu	325	330	335
Phe	Val	Phe	Leu	Ser	Val	Ile	Glu	Tyr	Ala	Ala	Val	Asn	Tyr	Leu	Thr	340	345	350
Thr	Val	Glu	Glu	Trp	Lys	Gln	Leu	Asn	Arg	Arg	Gly	Lys	Ile	Ser	Gly	355	360	365
Met	Tyr	Asn	Ile	Asp	Ala	Val	Gln	Ala	Met	Ala	Phe	Asp	Gly	Cys	Tyr	370	375	380

His Asp Gly Glu Thr Asp Val Asp Gln Thr Ser Phe Phe Leu His Ser
385 390 395 400

Glu Glu Asp Ser Met Arg Thr Lys Phe Thr Gly Ser Pro Cys Ala Asp
405 410 415

Ser Ser Gln Ile Lys Arg Lys Ser Leu Gly Gly Asn Val Gly Arg Ile
420 425 430

Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg Ile Val Phe
435 440 445

Pro Val Val Tyr Ile Ile Phe Asn Leu Phe Tyr Trp Gly Ile Tyr Val
450 455 460

<210> 37

<211> 464

<212> PRT

<213> Rattus norvegicus

<400> 37

Met Val Leu Ala Phe Trp Leu Ala Phe Phe Thr Tyr Thr Trp Ile Thr
1 5 10 15

Leu Met Leu Asp Ala Ser Ala Val Lys Glu Pro His Gln Gln Cys Leu
20 25 30

Ser Ser Pro Lys Gln Thr Arg Ile Arg Glu Thr Arg Met Arg Lys Asp
35 40 45

Asp Leu Thr Lys Val Trp Pro Leu Lys Arg Glu Gln Leu Leu His Ile
50 55 60

Glu Asp His Asp Phe Ser Thr Arg Pro Gly Phe Gly Gly Ser Pro Val
65 70 75 80

Pro Val Gly Ile Asp Val Gln Val Glu Ser Ile Asp Ser Ile Ser Glu
85 90 95

Val Asn Met Asp Phe Thr Met Thr Phe Tyr Leu Arg His Tyr Trp Lys
100 105 110

Asp Glu Arg Leu Ser Phe Pro Ser Thr Thr Asn Lys Ser Met Thr Phe
115 120 125

Asp Arg Arg Leu Ile Gln Lys Ile Trp Val Pro Asp Ile Phe Phe Val
130 135 140

His Ser Lys Arg Ser Phe Ile His Asp Thr Thr Val Glu Asn Ile Met
145 150 155 160

Leu Arg Val His Pro Asp Gly Asn Val Leu Phe Ser Leu Arg Ile Thr
165 170 175

Val Ser Ala Met Cys Phe Met Asp Phe Ser Arg Phe Pro Leu Asp Thr
180 185 190

Gln Asn Cys Ser Leu Glu Leu Glu Ser Tyr Ala Tyr Asn Glu Glu Asp
 195 200 205
 Leu Met Leu Tyr Trp Lys His Gly Asn Lys Ser Leu Asn Thr Glu Glu
 210 215 220
 His Ile Ser Leu Ser Gln Phe Phe Ile Glu Glu Phe Ser Ala Ser Ser
 225 230 235 240
 Gly Leu Ala Phe Tyr Ser Ser Thr Gly Trp Tyr Tyr Arg Leu Phe Ile
 245 250 255
 Asn Phe Val Leu Arg Arg His Ile Phe Phe Phe Val Leu Gln Thr Tyr
 260 265 270
 Phe Pro Ala Met Leu Met Val Met Leu Ser Trp Val Ser Phe Trp Ile
 275 280 285
 Asp Arg Arg Ala Val Pro Ala Arg Val Ser Leu Gly Ile Thr Thr Val
 290 295 300
 Leu Thr Met Ser Thr Ile Val Thr Gly Val Ser Ala Ser Met Pro Gln
 305 310 315 320
 Val Ser Tyr Val Lys Ala Val Asp Val Tyr Met Trp Val Ser Ser Leu
 325 330 335
 Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn Tyr Leu Thr
 340 345 350
 Thr Val Glu Glu Trp Lys Gln Leu Asn Arg Arg Gly Lys Ile Ser Gly
 355 360 365
 Met Tyr Asn Ile Asp Ala Val Gln Ala Met Ala Phe Asp Gly Cys Tyr
 370 375 380
 His Asp Gly Glu Thr Asp Val Asp Gln Thr Ser Phe Phe Leu His Ser
 385 390 395 400
 Glu Glu Asp Ser Met Arg Thr Lys Phe Thr Gly Ser Pro Cys Ala Asp
 405 410 415
 Ser Ser Gln Ile Lys Arg Lys Ser Leu Gly Gly Asn Val Gly Arg Ile
 420 425 430
 Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg Ile Val Phe
 435 440 445
 Pro Val Val Tyr Ile Ile Phe Asn Leu Phe Tyr Trp Gly Ile Tyr Val
 450 455 460

<210> 38

<211> 464

<212> PRT

<213> Rattus norvegicus

<400> 38

Met	Val	Leu	Ala	Phe	Trp	Leu	Ala	Phe	Phe	Thr	Tyr	Thr	Trp	Ile	Thr
1				5					10					15	
Leu	Met	Leu	Asp	Ala	Ser	Ala	Val	Lys	Glu	Pro	His	Gln	Gln	Cys	Leu
			20					25					30		
Ser	Ser	Pro	Lys	Gln	Thr	Arg	Ile	Arg	Glu	Thr	Arg	Met	Arg	Lys	Asp
		35					40					45			
Asp	Leu	Thr	Lys	Val	Trp	Pro	Leu	Lys	Arg	Glu	Gln	Leu	Leu	His	Ile
	50					55					60				
Glu	Asp	His	Asp	Phe	Ser	Thr	Arg	Pro	Gly	Phe	Gly	Gly	Ser	Pro	Val
65					70					75					80
Pro	Val	Gly	Ile	Asp	Val	Gln	Val	Glu	Ser	Ile	Asp	Ser	Ile	Ser	Glu
				85					90					95	
Val	Asn	Met	Asp	Phe	Thr	Met	Thr	Phe	Tyr	Leu	Arg	His	Tyr	Trp	Lys
			100					105					110		
Asp	Glu	Arg	Leu	Ser	Phe	Pro	Ser	Thr	Thr	Asn	Lys	Ser	Met	Thr	Phe
		115					120					125			
Asp	Arg	Arg	Leu	Ile	Gln	Lys	Ile	Trp	Val	Pro	Asp	Ile	Phe	Phe	Val
	130					135					140				
His	Ser	Lys	Arg	Ser	Phe	Ile	His	Asp	Thr	Thr	Val	Glu	Asn	Ile	Met
145					150					155					160
Leu	Arg	Val	His	Pro	Asp	Gly	Asn	Val	Leu	Phe	Ser	Leu	Arg	Ile	Thr
				165					170					175	
Val	Ser	Ala	Met	Cys	Phe	Met	Asp	Phe	Ser	Arg	Phe	Pro	Leu	Asp	Thr
			180					185					190		
Gln	Asn	Cys	Ser	Leu	Glu	Leu	Glu	Ser	Tyr	Ala	Tyr	Asn	Glu	Glu	Asp
		195					200					205			
Leu	Met	Leu	Tyr	Trp	Lys	His	Gly	Asn	Lys	Ser	Leu	Asn	Thr	Glu	Glu
	210					215					220				
His	Ile	Ser	Leu	Ser	Gln	Phe	Phe	Ile	Glu	Glu	Phe	Ser	Ala	Ser	Ser
225					230					235					240
Gly	Leu	Ala	Phe	Tyr	Ser	Ser	Thr	Gly	Trp	Tyr	Tyr	Arg	Leu	Phe	Ile
				245					250					255	
Asn	Phe	Val	Leu	Arg	Arg	His	Ile	Phe	Phe	Phe	Val	Leu	Gln	Thr	Tyr
			260					265				270			
Phe	Pro	Ala	Met	Leu	Met	Val	Met	Leu	Ser	Trp	Val	Ser	Phe	Trp	Ile
		275					280					285			
Asp	Arg	Arg	Ala	Val	Pro	Ala	Arg	Val	Ser	Leu	Gly	Ile	Thr	Thr	Val
	290					295					300				

Leu Thr Met Ser Thr Ile Val Thr Gly Val Ser Ala Ser Met Pro Gln
 305 310 315 320
 Val Ser Tyr Val Lys Ala Val Asp Val Tyr Met Trp Val Ser Ser Leu
 325 330 335
 Phe Val Phe Leu Ser Val Ile Glu Tyr Ala Ala Val Asn Tyr Leu Thr
 340 345 350
 Thr Val Glu Glu Trp Lys Gln Leu Asn Arg Arg Gly Lys Ile Ser Gly
 355 360 365
 Met Tyr Asn Ile Asp Ala Val Gln Ala Met Ala Phe Asp Gly Cys Tyr
 370 375 380
 His Asp Gly Glu Thr Asp Val Asp Gln Thr Ser Phe Phe Leu His Ser
 385 390 395 400
 Glu Glu Asp Ser Met Arg Thr Lys Phe Thr Gly Ser Pro Cys Ala Asp
 405 410 415
 Ser Ser Gln Ile Lys Arg Lys Ser Leu Gly Gly Asn Val Gly Arg Ile
 420 425 430
 Ile Leu Glu Asn Asn His Val Ile Asp Thr Tyr Ser Arg Ile Val Phe
 435 440 445
 Pro Val Val Tyr Ile Ile Phe Asn Leu Phe Tyr Trp Gly Ile Tyr Val
 450 455 460

<210> 39
 <211> 392
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (111)
 <223> Any amino acid

<400> 39
 Met Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr Ser Glu Arg Gln
 1 5 10 15
 Ala Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val
 20 25 30
 Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile
 35 40 45
 Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys
 50 55 60
 Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu
 65 70 75 80

Ala	Trp	Asn	Met	Ser	Glu	Cys	Gly	Gly	Leu	Cys	Gln	Pro	Thr	Glu	Tyr	85	90	95
Ser	Ala	Asp	Gly	Phe	Ala	Pro	Cys	Gln	Leu	Cys	Ala	Leu	Gly	Xaa	Phe	100	105	110
Gln	Pro	Glu	Ala	Gly	Arg	Thr	Ser	Cys	Phe	Pro	Cys	Gly	Gly	Gly	Leu	115	120	125
Ala	Thr	Lys	His	Gln	Gly	Ala	Thr	Ser	Phe	Gln	Asp	Cys	Glu	Thr	Arg	130	135	140
Val	Gln	Cys	Ser	Pro	Gly	His	Phe	Tyr	Asn	Thr	Thr	Thr	His	Arg	Cys	145	150	155
Ile	Arg	Cys	Pro	Val	Gly	Thr	Tyr	Gln	Pro	Glu	Phe	Gly	Lys	Asn	Asn	165	170	175
Cys	Val	Ser	Cys	Pro	Gly	Asn	Thr	Thr	Thr	Asp	Phe	Asp	Gly	Ser	Thr	180	185	190
Asn	Ile	Thr	Gln	Cys	Lys	Asn	Arg	Arg	Cys	Gly	Gly	Glu	Leu	Gly	Asp	195	200	205
Phe	Thr	Gly	Tyr	Ile	Glu	Ser	Pro	Asn	Tyr	Pro	Gly	Asn	Tyr	Pro	Ala	210	215	220
Asn	Thr	Glu	Cys	Thr	Trp	Thr	Ile	Asn	Pro	Pro	Pro	Lys	Arg	Arg	Ile	225	230	235
Leu	Ile	Val	Val	Pro	Glu	Ile	Phe	Leu	Pro	Ile	Glu	Asp	Asp	Cys	Gly	245	250	255
Asp	Tyr	Leu	Val	Met	Arg	Lys	Thr	Ser	Ser	Ser	Asn	Ser	Val	Thr	Thr	260	265	270
Tyr	Glu	Thr	Cys	Gln	Thr	Tyr	Glu	Arg	Pro	Ile	Ala	Phe	Thr	Ser	Arg	275	280	285
Ser	Lys	Lys	Leu	Trp	Ile	Gln	Phe	Lys	Ser	Asn	Glu	Gly	Asn	Ser	Ala	290	295	300
Arg	Gly	Phe	Gln	Val	Pro	Tyr	Val	Thr	Tyr	Asp	Glu	Asp	Tyr	Gln	Glu	305	310	315
Leu	Ile	Glu	Asp	Ile	Val	Arg	Asp	Gly	Arg	Leu	Tyr	Ala	Ser	Glu	Asn	325	330	335
His	Gln	Glu	Ile	Leu	Lys	Asp	Lys	Lys	Leu	Ile	Lys	Ala	Leu	Phe	Asp	340	345	350
Val	Leu	Ala	His	Pro	Gln	Asn	Tyr	Phe	Lys	Tyr	Thr	Ala	Gln	Glu	Ser	355	360	365
Arg	Glu	Met	Phe	Pro	Arg	Ser	Phe	Ile	Arg	Leu	Leu	Arg	Ser	Lys	Val	370	375	380

Ser Arg Phe Leu Arg Pro Tyr Lys
385 390

<210> 40

<211> 283

<212> PRT

<213> Rattus norvegicus

<400> 40

Glu Val Asn Gly Ile Leu Met Ser Lys Leu Met Ser Asp Asn Trp Asp
1 5 10 15

Lys Ile Trp Asn Phe Gln Ala Lys Pro Asp Asp Leu Leu Ile Ala Thr
20 25 30

Tyr Ala Lys Ala Gly Thr Thr Trp Thr Gln Glu Ile Val Asp Met Ile
35 40 45

Gln Asn Asp Gly Asp Val Gln Lys Cys Gln Arg Ala Asn Thr Tyr Asp
50 55 60

Arg His Pro Phe Ile Glu Trp Thr Leu Pro Ser Pro Leu Asn Ser Gly
65 70 75 80

Leu Asp Leu Ala Asn Lys Met Pro Ser Pro Arg Thr Leu Lys Thr His
85 90 95

Leu Pro Val His Met Leu Pro Pro Ser Phe Trp Lys Glu Asn Ser Lys
100 105 110

Ile Ile Tyr Val Ala Arg Asn Ala Lys Asp Cys Leu Val Ser Tyr Tyr
115 120 125

Tyr Phe Ser Arg Met Asn Lys Met Leu Pro Asp Pro Gly Thr Leu Gly
130 135 140

Glu Tyr Ile Glu Gln Phe Lys Ala Gly Lys Val Leu Trp Gly Ser Trp
145 150 155 160

Tyr Asp His Val Lys Gly Trp Trp Asp Val Lys Asp Gln His Arg Ile
165 170 175

Leu Tyr Leu Phe Tyr Glu Asp Met Lys Glu Asp Pro Lys Arg Glu Ile
180 185 190

Lys Lys Ile Ala Lys Phe Leu Glu Lys Asp Ile Ser Glu Glu Val Leu
195 200 205

Asn Lys Ile Ile Tyr His Thr Ser Phe Asp Val Met Lys Glu Asn Pro
210 215 220

Met Ala Asn Tyr Thr Thr Leu Pro Ser Ser Ile Met Asp His Ser Ile
225 230 235 240

Ser Pro Phe Met Arg Lys Gly Met Pro Gly Asp Trp Lys Asn Tyr Phe
245 250 255

Thr Val Ala Gln Ser Glu Asp Phe Asp Glu Asp Tyr Arg Arg Lys Met
 260 265 270

Ala Gly Ser Asn Ile Thr Phe Arg Thr Glu Ile
 275 280

<210> 41

<211> 285

<212> PRT

<213> Homo sapiens

<400> 41

Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln Tyr Asp
 1 5 10 15

Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His Glu Asp
 20 25 30

Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg Asp Ile
 35 40 45

Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asp Val Lys Arg
 50 55 60

Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg Leu Ser
 65 70 75 80

Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys Ala Arg
 85 90 95

Gly Glu Val Ile His Cys Lys Leu Arg Ala Met Lys Glu Leu Ser Glu
 100 105 110

Ala Ala Glu Ala Gln His Gly Pro His Ser Ala Val Ala Arg Ile Ser
 115 120 125

Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala Met His
 130 135 140

Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys Ile Arg
 145 150 155 160

Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly Asp Gln
 165 170 175

Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser Glu Asn
 180 185 190

Leu Leu Ala Asp Val Lys Gly Ala Arg Ala Ala Leu Asn Glu Ile Glu
 195 200 205

Ser Arg His Arg Glu Leu Leu Arg Leu Glu Ser Arg Ile Arg Asp Val
 210 215 220

His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln Ala Asp
 225 230 235 240

Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp Tyr Thr
245 250 255

Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu Glu Lys
260 265 270

Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys
275 280 285

<210> 42

<211> 285

<212> PRT

<213> Homo sapiens

<400> 42

Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln Tyr Asp
1 5 10 15

Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His Glu Asp
20 25 30

Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg Asp Ile
35 40 45

Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asp Val Lys Arg
50 55 60

Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg Leu Ser
65 70 75 80

Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys Ala Arg
85 90 95

Gly Glu Val Ile His Cys Lys Leu Arg Ala Met Lys Glu Leu Ser Glu
100 105 110

Ala Ala Glu Ala Gln His Gly Pro His Ser Ala Val Ala Arg Ile Ser
115 120 125

Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala Met His
130 135 140

Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys Ile Arg
145 150 155 160

Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly Asp Gln
165 170 175

Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser Glu Asn
180 185 190

Leu Leu Ala Asp Val Lys Gly Ala Arg Ala Ala Leu Asn Glu Ile Glu
195 200 205

Ser Arg His Arg Glu Leu Leu Arg Leu Glu Ser Arg Ile Arg Asp Val
210 215 220

His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln Ala Asp
 225 230 235 240

Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp Tyr Thr
 245 250 255

Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu Glu Lys
 260 265 270

Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys
 275 280 285

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 43

ttggaagaga tggtcctggc tttc

24

<210> 44

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 44

ttcataggat tctcagctgt gtgagt

27

<210> 45

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 45

ttggaagaga tggtcctggc tttc

24

<210> 46

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 46
ttcataggat tctcagctgt gtgagtg 27

<210> 47
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 47
gtgtgttcct ctcgactgtg ga 22

<210> 48
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 48
gacccttgga ccctacttca aa 22

<210> 49
<211> 24
<212> DNA
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